RAW SEQUENCE LISTING   DATE: 08/09/2001
PATENT APPLICATION: US/09/730,559B   TIME: 12:36:41

Input Set : **A:\766.21 CIP Sequence.txt**
Output Set: **N:\CRF3\08092001\I730559B.raw**

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 4 <110> APPLICANT: ISHIWATA, TETSUYOSHI
 5        SAKURADA, MIKIKO
 6        KAWABATA, AYAKO
 7        NAKAGAWA, SATOSHI
 8        NISHI, TATSUNARI
 9        KUGA, TETSURO
10        SAWADA, SHIGEMASA
11        TAKEI, MASAMI
12        SHIBATA, KENJI
13        FURUYA, AKIKO
15 <120> TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
17 <130> FILE REFERENCE: 766.21 CIP
19 <140> CURRENT APPLICATION NUMBER: US 09/730,559B
20 <141> CURRENT FILING DATE: 2000-12-07
22 <160> NUMBER OF SEQ ID NOS: 121
24 <170> SOFTWARE: PatentIn Ver. 2.0
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27 <211> LENGTH: 4276
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (53)..(742)
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38                                                               1
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41 Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly
42           5                   10                  15
44 ctg ggt tca cct cac tgc ttc agt cac cag aat ggg gag aga gtg gaa   154
45 Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu
46          20                  25                  30
48 cga tat tct cga aag gtg ttt gta ggc gga ttg cct cca gac att gat   202
49 Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp
50 35                  40                  45                  50
52 gaa gat gag atc aca gct agt ttt cgt cgc ttt ggc cct ctg att gtg   250
53 Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val
54                  55                  60                  65
56 gat tgg cct cat aaa gct gag agc aaa tcc tat ttt cct cct aaa ggc   298
57 Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly
58                  70                  75                  80
60 tat gca ttc ctg ctg ttt caa gat gaa agc tct gtg cag gct ctc att   346
61 Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile
62          85                  90                  95
64 gat gca tgc att gaa gaa gat gga aaa ctc tac ctt tgt gta tca agt   394
65 Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser
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68 ccc act atc aag gat aag cca gtc cag att cgg cct tgg aat ctc agt    442
69 Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser
70 115                     120                     125                     130
72 gac agt gac ttt gtg atg gat ggt tca cag cca ctt gac cca cga aaa    490
73 Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys
74                     135                     140                     145
76 act ata ttt gtt ggt ggt gtt cct cga cca tta cga gct gtg gag ctt    538
77 Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu
78                     150                     155                     160
80 gcg atg gta atg gat cgg cta tac gga ggt gtg tgc tac gct ggg att    586
81 Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile
82           165                     170                     175
84 gat acc gac cct gag cta aaa tac cca aaa gga gct ggg aga gtt gcg    634
85 Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala
86           180                     185                     190
88 ttc tct aat caa cag agt tac ata gct gct atc agt gcc cgc ttt gtt    682
89 Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val
90 195                     200                     205                     210
92 cag ctg cag cat gga gag ata gat aaa cgg gta agc ctt ata cta cat    730
93 Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His
94                     215                     220                     225
96 ttt gga aaa ttc tagaaatggt cctctaaatg tgtgattacc aatattagaa    782
97 Phe Gly Lys Phe
98                     230
100 cgggagcatt ttatgacaat aaagtgacag ctgacaattt tgcctataga gttaattatg 842
102 gtctataata catgaaataa tgtcctatga atttctttta tctttcagtt ttttgagtag 902
104 cctaatcaga acactacaat ttacttgagt taatttaatc ttctctaact tccattcaat 962
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128 aattcaagat gtaaaaatca tcaagtcagt agcagttttt gctttttatg tttcatgtca 1682
130 tgtacagtct acttcactgg cagtaaaaaa atttaagata gtggtggtca tcctacaaac 1742
132 tgtgaatcta ttaaagagaa aagtatctgt tctattctaa gcatggggga gggacaagat 1802
134 tagtatgtta acatgcctac tttgtttgtt tgagatggag tctctctccg tcacccaggc 1862
136 tggagtgcag tggtacagtc tcagctcact ccaacctctg cctcccgggt tcaagtgatt 1922
138 ctcctgcctt agcctcccga gtaggtggaa ttacaggcat ataccaccat gcccaacaaa 1982
140 tgtttgtatt tttagtggag acagggtttc accgtgttgg tcaggccagt ttcaaactcc 2042
142 tgacctcaag ggatccacct gcctcacccc ctcaaagtgc tgggattaca ggcatgagcc 2102
144 acccaccatg cctggcctac ttggtttttt atgcacacta aaaatacct acatctcact 2162
146 gccttattcc aacataagtt tcagagctgt gggattggtc attagaaatt cagactgaat 2222
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152 gacactcttc ttctcctttt gtacttttat ttttttagtt aaaaaatttt ttttagaggg 2402
154 agggtctcac tctgtcaccc aggctggagc acagaatcac aatcatgact cactgcatgt 2462
156 tcttctcctt ttgttcatgg ctaatcttgg tcaggattcc ttgtcagagc tgggtggcac 2522
158 cagtgctggt gacagcctgc tgtaagggag tttcagccat gaatctctcc agactaaaaa 2582
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164 gactttttaga ctcaggtgaa ccattcttac tgagaaagaa caaagcaggg ttttagactg 2762
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182 tttgggcacc ttggaacaga ttcattcaga tagtgggtgg aaatgtacat gtatggtaag 3302
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202 caaacttcct gcaacatttt cttagaggag agagagaaat attaaaagag aaatgaaaca 3902
204 atagagtatt ttgggttttt aattaaatta ttgttaataa tataacatat aagaatactt 3962
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216 aaaaaaaaaa aaaa                                                    4276
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222 <213> ORGANISM: Homo sapiens
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225 <221> NAME/KEY: CDS
226 <222> LOCATION: (107)..(535)
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232                                                      Met Gly Ser
233                                                        1
235 gac aaa aga gtg agt aga aca gag cgt agt gga aga tac ggt tcc atc  163
236 Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile
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Input Set : A:\766.21 CIP Sequence.txt
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240 Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg
241  20                   25                   30                   35
243 gac tca gat tac aaa aga tct agt gat gat cgg agg ggt gat aga tat  259
244 Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr
245                  40                   45                   50
247 gat gac tac cga gac tat gac agt cca gag aga gag cgt gaa aga agg  307
248 Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg
249                  55                   60                   65
251 aac agt gac cga tcc gaa gat ggc tac cat tca gat ggt gac tat ggt  355
252 Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly
253          70                   75                   80
255 gag cac gac tat agg cat gac atc agt gac gag agg gag agc aag acc  403
256 Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr
257      85                   90                   95
259 atc atg ctg cgc ggc ctt ccc atc acc atc aca gag agc gat att cga  451
260 Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg
261 100                  105                  110                  115
263 gaa atg atg gag tcc ttc gaa ggc cct cag cct gcg gat gtg agg ctg  499
264 Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu
265                  120                  125                  130
267 atg aag agg aaa aca ggt gag agc ttg ctt agt tcc tgatattatt       545
268 Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser
269                  135                  140
271 gttctcttcc ccattcccac ctcagtccct aaagaacatc ctgattcccc cagtcttcaa  605
273 gcacatgaat tcagaatgaa aggtttgcca tggctaagga atgtgactct ttgaaaacca  665
275 tgttagcatc tgaggaactt ttttaaactt tgttttaggg acttttttt cccttaggtaa  725
277 gtaatgattt ataaactcct tttttttttt ttgactatag tcggttgcat ggttacttta  785
279 agcgtggaat caaatggagt ggcatttagt tcaggcggct tgttccttgc catggcaaag  845
281 tatcaagaag atccccaagt caagtcacat ttgtaaagct gcttcccaat tggctttgtc  905
283 acgcagtgtt gaagcagtgg gagagagatt cacctgttat aaaggaactg actaacacaa  965
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295 aaacatggct acctacctgg cagggctttg ttaactactg aatacctgtc tggtaatcac 1325
297 taaaacatct taatgtttcc cttttttcta gtttgttata ttcctattat gtccattgag 1385
299 agtaagctta gtatatcaaa ctctccattt gacagtgaag agaacatagt gaaagtctgt 1445
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303 cgtaactgct cagaccggtc ttcagggaat atttaaggac ttagtggaat ttatgaacaa 1565
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307 gcattaacat tctaatctcc ttgagaatgc cttttatagt ctgttcaaag caagtcattg 1685
309 atggttcttc gaggtagtgt taactgaagt gttcttcagt ttgtcaagat aatgttcagt 1745
311 gcttggcact aaataacat tttttgcaag aactccaagg cacattattg aatgccttta 1805
313 accaagtgca ttctgggaag tttgcttgac tcattatctt gcttttctgc agcattctgt 1865
315 gatttgagtc atccatgaat ccatgaataa aagttacatt ctttgattgg taatattgcc 1925
317 atttataaca agactcacta atgagggtat cactttgact gactgatttg ttaaagtttt 1985
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Input Set : A:\766.21 CIP Sequence.txt
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321 attcatttca taccatagat accatcctag taaatccaga acatatacaa ggttcatgtg 2105
323 agtctgcttt cttgacatga tagcattgtt tgatgcagtg gatatgtcag aatgactaac 2165
325 ctaggagttt aaaactccta agaaactaaa acctgtaaga catttaaaag tctccacaat 2225
327 tttaatgtat acaaagctat gttactgtgt aacacattac agttcaaatt cactccagaa 2285
329 ataaaaggcc agtaggatta gggactcact ggtagtttgg agtctcccag cacacatccc 2345
331 tcctagtggg atgatctatt cacatatctc ccagcttttt tattttgct tctgtatatc 2405
333 acagtgagtg gatggccctt cagcttttc tctcctggcc agacatgcag tcttgccttt 2465
335 agatatcgca gagacaaaat tcacagcatg tcttaaatct tccaggattt gcaagaacca 2525
337 aattgctcaa cagtatgtat gtttagaggg gttagactcc tttttaaaat ctggatatct 2585
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344 <210> SEQ ID NO: 3
345 <211> LENGTH: 2981
346 <212> TYPE: DNA
347 <213> ORGANISM: Homo sapiens
349 <220> FEATURE:
350 <221> NAME/KEY: CDS
351 <222> LOCATION: (1297)..(1608)
353 <400> SEQUENCE: 3

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358 gctgggacaa caggcacctg ccaccacgcc cggctaattt tttgtatttt tagtagagac 180
360 agggtttcac catgttagcc aggatggtct caatctcctg acctcgtgat ccacccgcct 240
362 cagcctccca aagtgctgag attacaggtg tgagccacca cgcccagcca catctttctt 300
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394 agtctggaat ttgggtatat gttggacaga ggctgcctaa gtgaccagct tcaacaacag 1260
396 ccctgggtgc tgggtcactc atgacccata gacaaa atg cca cac atg ttg tca  1314
397                                             Met Pro His Met Leu Ser
398                                             1               5
400 cag ctt att gct gga gga gtt agc aca tcc tgt gtg act gca ctg gga  1362
401 Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys Val Thr Ala Leu Gly
402             10              15              20
404 gag gaa act ggt gcc tgg ttc cct gtg tat ttg tcc cac gcc tcc agt  1410
405 Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu Ser His Ala Ser Ser
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VERIFICATION SUMMARY   DATE: 08/09/2001
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L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115
L:2863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:2917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
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